



Figure 4a. 158P1D7 amino acid BLAST homology to hypothetical protein FLJ22774.

Identities = 798/798 (100%)

Query: 44 MLINEAKGIKMVSEISVPPSRPFQLSLLNNGLTMLHTNDFSGLTNAISIH LGFN NIADI 103
MLINCEAKGIKMVSEISVPPSRPFQLSLLNNGLTMLHTNDFSGLTNAISIH LGFN NIADI
Sbjct: 1 MLINEAKGIKMVSEISVPPSRPFQLSLLNNGLTMLHTNDFSGLTNAISIH LGFN NIADI 60

Query: 104 EIGAFNGLG L L K Q L H I N H N S L E I L K E D T F H G L E N L E F L Q A D N N F I T V I E P S A F S K L N R L K 163
EIGAFNGLG L L K Q L H I N H N S L E I L K E D T F H G L E N L E F L Q A D N N F I T V I E P S A F S K L N R L K
Sbjct: 61 EIGAFNGLG L L K Q L H I N H N S L E I L K E D T F H G L E N L E F L Q A D N N F I T V I E P S A F S K L N R L K 120

Query: 164 V L I L N D N A I E S L P P N I F R F V P L T H L D L R G N Q L Q T L P Y V G F L E H I G R I L D L Q L E D N K W A C N 223
V L I L N D N A I E S L P P N I F R F V P L T H L D L R G N Q L Q T L P Y V G F L E H I G R I L D L Q L E D N K W A C N
Sbjct: 121 V L I L N D N A I E S L P P N I F R F V P L T H L D L R G N Q L Q T L P Y V G F L E H I G R I L D L Q L E D N K W A C N 180

Query: 224 C D L L Q L K T W L E N M P P Q S I I G D V V C N S P P F F K G S I L S R L K K E S I C P T P P V Y E E H E D P S G S L 283
C D L L Q L K T W L E N M P P Q S I I G D V V C N S P P F F K G S I L S R L K K E S I C P T P P V Y E E H E D P S G S L
Sbjct: 181 C D L L Q L K T W L E N M P P Q S I I G D V V C N S P P F F K G S I L S R L K K E S I C P T P P V Y E E H E D P S G S L 240

Query: 284 H L A A T S S I N D S R M S T K T T S I L K L P T K A P G L I P Y I T K P S T Q L P G P Y C P I P C N C K V L S P S G L 343
H L A A T S S I N D S R M S T K T T S I L K L P T K A P G L I P Y I T K P S T Q L P G P Y C P I P C N C K V L S P S G L
Sbjct: 241 H L A A T S S I N D S R M S T K T T S I L K L P T K A P G L I P Y I T K P S T Q L P G P Y C P I P C N C K V L S P S G L 300

Query: 344 L I H C Q E R N I E S L S D L R P P P Q N P R K L I L A G N I I H S L M K S D L V E Y F T L E M L H L G N N R I E V L E 403
L I H C Q E R N I E S L S D L R P P P Q N P R K L I L A G N I I H S L M K S D L V E Y F T L E M L H L G N N R I E V L E
Sbjct: 301 L I H C Q E R N I E S L S D L R P P P Q N P R K L I L A G N I I H S L M K S D L V E Y F T L E M L H L G N N R I E V L E 360

Query: 404 E G S F M N L T R L Q K L Y L N G N H L T K L S K G M F L G L H N L E Y L Y L E Y N A I K E I L P G T F N P M P K L K V 463
E G S F M N L T R L Q K L Y L N G N H L T K L S K G M F L G L H N L E Y L Y L E Y N A I K E I L P G T F N P M P K L K V
Sbjct: 361 E G S F M N L T R L Q K L Y L N G N H L T K L S K G M F L G L H N L E Y L Y L E Y N A I K E I L P G T F N P M P K L K V 420

Query: 464 L Y L N N N L L Q V L P P H I F S G V P L T K V N L K T N Q F T H L P V S N I L D D L D L L T Q I D L E D N P W D C S C 523
L Y L N N N L L Q V L P P H I F S G V P L T K V N L K T N Q F T H L P V S N I L D D L D L L T Q I D L E D N P W D C S C
Sbjct: 421 L Y L N N N L L Q V L P P H I F S G V P L T K V N L K T N Q F T H L P V S N I L D D L D L L T Q I D L E D N P W D C S C 480

Query: 524 D L V G L Q Q W I Q K L S K N T V T D D I L C T S P G H L D K K E L K A L N S E I L C P G L V N N P S M P T Q T S Y L M 583
D L V G L Q Q W I Q K L S K N T V T D D I L C T S P G H L D K K E L K A L N S E I L C P G L V N N P S M P T Q T S Y L M
Sbjct: 481 D L V G L Q Q W I Q K L S K N T V T D D I L C T S P G H L D K K E L K A L N S E I L C P G L V N N P S M P T Q T S Y L M 540

Query: 584 V T T P A T T T N T A D T I L R S L T D A V P L S V L I L G L L I M F I T I V F C A A G I V V L V L H R R R R Y K K K Q 643
V T T P A T T T N T A D T I L R S L T D A V P L S V L I L G L L I M F I T I V F C A A G I V V L V L H R R R R Y K K K Q
Sbjct: 541 V T T P A T T T N T A D T I L R S L T D A V P L S V L I L G L L I M F I T I V F C A A G I V V L V L H R R R R Y K K K Q 600

Query: 644 V D E Q M R D N S P V H L Q Y S M Y G H K T T H H T T E R P S A S L Y E Q H M V S P M V H V Y R S P S F G P K H L E E E 703
V D E Q M R D N S P V H L Q Y S M Y G H K T T H H T T E R P S A S L Y E Q H M V S P M V H V Y R S P S F G P K H L E E E
Sbjct: 601 V D E Q M R D N S P V H L Q Y S M Y G H K T T H H T T E R P S A S L Y E Q H M V S P M V H V Y R S P S F G P K H L E E E 660

Query: 704 E E R N E K E G S D A K H L Q R S L L E Q E N H S P L T G S N M K Y K T T N Q S T E F L S F Q D A S S L Y R N I L E K E 763
E E R N E K E G S D A K H L Q R S L L E Q E N H S P L T G S N M K Y K T T N Q S T E F L S F Q D A S S L Y R N I L E K E
Sbjct: 661 E E R N E K E G S D A K H L Q R S L L E Q E N H S P L T G S N M K Y K T T N Q S T E F L S F Q D A S S L Y R N I L E K E 720

Query: 764 R E L Q Q L G I T E Y L R K N I A Q L Q P D M E A H Y P G A H E E L K L M E T L M Y S R P R K V L V E Q T K N E Y F E L 823
R E L Q Q L G I T E Y L R K N I A Q L Q P D M E A H Y P G A H E E L K L M E T L M Y S R P R K V L V E Q T K N E Y F E L
Sbjct: 721 R E L Q Q L G I T E Y L R K N I A Q L Q P D M E A H Y P G A H E E L K L M E T L M Y S R P R K V L V E Q T K N E Y F E L 780

Figure 4b

Query: 824 KANLHAEPDYLEVLEQQT 841 (SEQ ID NO:657)
KANLHAEPDYLEVLEQQT
Sbjct: 781 KANLHAEPDYLEVLEQQT 798 (SEQ ID NO:658)

Figure 5a: Alignment of 158P1D7 with human FLJ22774, CLONE KAIA1575. [Homo sapiens]

Identities = 405/415 (97%), Positives = 405/415 (97%)

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158P1D7: 44 MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI 103
              MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI
Sbjct: 1      MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI 60

158P1D7:104 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 163
              EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK
Sbjct: 61     EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 120

158P1D7:164 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPLYVGFLEHIGRILDQLEDNKWACN 223
              VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPLYVGFLEHIGRILDQLEDNKWACN
Sbjct: 121    VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPLYVGFLEHIGRILDQLEDNKWACN 180

158P1D7:224 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL 283
              CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL
Sbjct: 181    CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL 240

158P1D7:284 HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 343
              HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL
Sbjct: 241    HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 300

158P1D7:344 LIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVL 403
              LIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVL
Sbjct: 301    LIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVL 360

158P1D7:404 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHXXXXXXXXXXAIKEILPGTFNPM 458 (SEQ ID NO:657)
              EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLH AIKEILPGTFNPM
Sbjct: 361    EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAIKEILPGTFNPM 415 (SEQ ID
              NO:659)

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Figure 5b: Alignment of 158P1D7 protein with a human protein similar to IGFALS

Identities = 316/864 (36%), Positives = 459/864 (52%)

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158P1D7:1  MKLWIHLFYSSLLACISLHSQTPVLSSRGSCDSLNCCEKDGTMLINCEAKGIKMVSEIS 60
              M L W+ L S+L++ + S V ++C+C + + +NCE + +++
Sbjct: 17  MFLWLFLILSALISSTNADSDISV-----EICNVCSVSVENVLYVNCEKVSRYRPNQLK 71

158P1D7:61 VPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADIEIGAFNGLGLLKQLHIN 120
              P S + L+ NN L +L+ N F ++A+S+HLG N + +IE GAF GL LKQLH+N
Sbjct: 72  PPWSNFYHLNFQNNFLNLYPNTFLNFHAVSLHLGNNKLQNIIEGGAFLGLSALKQLHLN 131

158P1D7:121 HNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLKVLILNDNAIESLPPNIF 180
              +N L+IL+ DTF G+ENLE+LQAD N I IE AF+KL++LKVLI LNDN I LP NIF
Sbjct: 132  NNELKILRADTFILGIENLEYLQADYNLIKYIERGAFNKLHLKVLILNDNLISFLPDNIF 191

158P1D7:181 RFVPLTHLDLRGNQLQTLPLYVGFLEHIGRILDQLEDNKWACNCDLLQLKTWLENMPPQS 240
              RF LTHLD+RGN++Q LPY+G LEHIGR+++LQLEDN W C+CDLL LK WLENMP
Sbjct: 192  RFASLTHLDIRGNRIQKLPYIGVLEHIGRVVELQLEDNPWNCSCDLLPLKAWLENMPYNI 251

158P1D7:241 IIGDVVCNSPPFFKGSILSRKKESICP-----TPPVYEEHEDPSGSLHLAATS 289
              IG+ +C +P G +L K+ +CP PP E+ + + H TS
Sbjct: 252  YIGEACETPSDLYGRLLKETNKQELCPMG TGSDFDVRILPPSQLENGYTTPNGHTTQTS 311

158P1D7:290 SINDSRMSTKTTSSILKLPTKAPGLI-----PYITKPSTQLPG-PYCPIPCCKV- 337
              KTT+ P+K G++ I T++P CP PC CK
Sbjct: 312  LHRLVTKPPKTTN---PSKISGIVAGKALSNRNLSQIVSYQTRVPPLTPCPAPCFCKTH 367

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158P1D7:338 LSPSGLLIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNN 397
S GL ++CQE+NI+S+S+L P P N +KL + GN I + SD ++ L++LHLG+N
Sbjct: 368 PSDLGLSVNCQEKNIQSMSELIPKPLNAKKLHVNGNSIKDQDVSDFTDFEGLDLLHLGNS 427

158P1D7:398 RIEVLEEGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHXXXXXXXXXXXXAIKEILPGTFNP 457
+I V++ F NLT L++LYLNGN + +L +F GLH IKEI GTF+
Sbjct: 428 QITVIKGDVVFHNLTNLRRLYLNGNQIERLYPEIFSGLHNLQYLYLEYNLIKEISAGTFDS 487

158P1D7:458 MXXXXXXXXXXXXXXXXXHI FSGVPLTKVNLKTNQFTHLPVSNIXXXXXXXXXXXXXXXXXN 517
M +IFSG PL ++NL+ N+F +LPVS + N
Sbjct: 488 MPNLQLLYLNNLLKSLPVYIFSGAPLARLNLNRNNKFMYPVSGVLDQLQSLTQIDLEGN 547

158P1D7:518 PWDCSCDLVGLQQWIOKLSKNTVTDDILCTSPGHLDDKKELKALNSEILCPGLVNNPSMPT 577
PWDC+CDLV L+ W++KLS V ++ C +P ELK+L +EILCP L+N PS P
Sbjct: 548 PWDCTCDLVALKLWVEKLSDGIVVKELKCETPVQFANIELKSLKNEILCPKLLNKPSAP- 606

158P1D7:578 QTSYLMVXXXXXXXXXXXXXILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVLRHRR 637
+ I VPLS+LIL +L++ I VF A ++V VL R +
Sbjct: 607 ---FTSPAPAITFTTPLGPIRSPPGGPVPLSILILSVLILTVFVAFCLLVFVLRNK 663

158P1D7:638 RYKKKQVDEQMRDNSPVHLQYSMYGHKTTHTTTERPSASLYEQHMVSPMVHVYRSPSFGP 697
+ K D + LQ + HK T + E + + +S + G
Sbjct: 664 KPTVKHEGLGNPDCGSMQLQLRKHDHK-----TNKKDGLSTEAFIPQTIEQMSKSHTCGL 718

158P1D7:698 KHLXXXXXXXXXXGSDAKHLQRSLLQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYR 757
K G K + R++ ++E + + T ++ E +D++ +
Sbjct: 719 KESETGFMFSDPPGQ--KVMRNVADKEKDLLHVDTRKRLSTIDELDELFP SRDSNVFIQ 776

158P1D7:758 NILEKERELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTK 817
N LE ++E +G++ + E YP + K ++L+ K++VEQ K
Sbjct: 777 NFLESKKEYNSIGVSGF-----EIRYPEKQPDKKSKKSLIGGNHISKIVVEQRK 824

158P1D7:818 NEYFELKANLHAEPDYLEVLEQQT 841 (SEQ ID NO:657)
+EYFELKA L + PDYL+VLE+QT
Sbjct: 825 SEYFELKAKLQSSPDYLQVLEEQT 848 (SEQ ID NO:660)